

SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> A novel polypeptide, a cDNA encoding the polypeptide and utilization thereof

<130> Q61531

<140>

<141>

<150> PCT/JP99/02284

<151> 1999-04-28

<150> JP HEI 10-119731

<151> 1998-04-28

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 1344

<212> DNA

<213> Mus musculus

<400> 1

atgccaggat taaaaaggat actcaactgtt accatcttgg cactctggct tccacatcct 60
ggaatgcac agcagcagtg cacaacgc tttgacctgg accggcagtc aggacagtgt 120
ctagatattt atgaatgccc gaccatccct gaggcttgcgttgggacat gatgtgtgtc 180
aaccagaatg gcgggtattt gtgcattccct cgaaccaacc cagtgtatcg agggcttac 240
tcaaattccct actctacatc ctactcaggc ccataccag cagcggcccc accagtacca 300
gcttccaact accccacgt ttcaaggcct cttgtctgcc gctttgggta tcagatggat 360
gaaggcäacc agtgtgtgga tgtggacgag tgtgcaacag actcacacca gtgcaaccct 420
accaggatct gatatcaacac tgaaggaggat tacacctgct cctgcacccga tgggtactgg 480
cttcttggaaag ggcagtgcct agatattgtat gaatgtcgct atggttactg ccagcagctc 540
tgtgcaaatg ttccaggatc ctattccctgt acatgcaacc ctggtttac cctcaacgc 600
gatggaaaggat cttgccaaga tgtgaacgag tgcgaaactg agaatccctg tggtcagacc 660
tgtgtcaaca cctatggctc tttcatctgc cgctgtgacc caggatatga acttgaggaa 720
gatggcattc actgcagtga tatggacgag tgcagctct ccgagttcct ctgtcaacac 780
gagtgtgtga accagccggg ctcataacttc tgctcgtgcc ctccaggcta cgctctgtt 840
gatgataacc gaagctgcca gatatcaat gaatgtgagc accgaaacca cacgtgtacc 900
tcactgcaga cttgtacaa tctacaaggg ggcttcaa atgttgcattt catcagctgt 960
gaggagcctt atctgctgat tggtaaaaac cgctgtatgt gtcctgtga gcacaccagc 1020
tgcagagacc agccattcac catcctgtat cgggacatgg atgtgggtgc aggacgctcc 1080
gttcctgttgc acatcttcca gatgcaagca acaacccatc accctggtgc ctattacatt 1140
ttccagatca aatctggcaa cgagggtcga gagttctata tgccggcaac agggcctatc 1200

agtgccaccc tggatgac acgccccatc aaagggcctc gggacatcca gctggacttg 1260
gagatgatca ctgtcaacac tgtcatcaac ttcagaggca gctccgtat ccgactgcgg 1320
atatatgtgt cgcatatcc gttc 1344

<210> 2
<211> 2233
<212> DNA
<213> Mus musculus

<220>
<223> Clone mouse A55 derived from Day 13 mouse
embryonic heart

<220>
<221> CDS
<222> (75)..(1418)

<220>
<221> sig_peptide
<222> (75)..(143)

<220>
<221> mat_peptide
<222> (144)..(1418)

<400> 2
aattcggcac gagcccaagt cccaccgcag agcctgcctt cctcgcgtcg ctttcctcc 60

cgcgcatctt ggat atg cca gga tta aaa agg ata ctc act gtt acc atc 110
Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
-20 -15

ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca 158
Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
-10 -5 -1 1 5

aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206
Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
10 15 20

gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc 254
Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
25 30 35

aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302
Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
40 45 50

cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac			350
Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr			
55	60	65	
cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca			398
Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser			
70	75	80	85
agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag			446
Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln			
90	95	100	
tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct			494
Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro			
105	110	115	
acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc acc			542
Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr			
120	125	130	
gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt			590
Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys			
135	140	145	
cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat			638
Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr			
150	155	160	165
tcc tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tct			686
Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser			
170	175	180	
tgc caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc			734
Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr			
185	190	195	
tgt gtc aac acc tat ggc tct ttc atc tgc cgc tgt gac cca gga tat			782
Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr			
200	205	210	
gaa ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc agc			830
Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser			
215	220	225	
ttc tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca			878
Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser			
230	235	240	245

tac ttc tgc tgc cct cca ggc tac gtc ctg ttg gat gat aac cga	926		
Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg			
250	255	260	
agc tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc	974		
Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr			
265	270	275	
tca ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat	1022		
Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Phe Lys Cys Ile Asp			
280	285	290	
ccc atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac cgc tgt	1070		
Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys			
295	300	305	
atg tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc	1118		
Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile			
310	315	320	325
ctg tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac	1166		
Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp			
330	335	340	
atc ttc cag atg caa gca aca acc cga tac cct ggt gcc tat tac att	1214		
Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile			
345	350	355	
ttc cag atc aaa tct ggc aac gag ggt cga gag ttc tat atg cgg caa	1262		
Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln			
360	365	370	
aca ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg	1310		
Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly			
375	380	385	
cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc	1358		
Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val			
390	395	400	405
atc aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tcg	1406		
Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser			
410	415	420	
cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag	1458		
Gln Tyr Pro Phe			
425			

caccgaggga cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac 1518
cttcctgct gaatatctcc tgggggcac agcctagcat cttgaccat atctgtacta 1578
ttgcagatgg tcactctgaa ggacaccctg ccctcagttc ctatgtgca gttatccaaa 1638
agtgttcatc ttagcccctg atatgaggtt gccagtgact cttcaaagcc ttccatttat 1698
ttccatcggt ttataaaaaa gaaaatagat tagatttgct ggggtatgag tcctcgaagg 1758
ttcaaaagac tgagtggctt gctctcacct cttcctctcc ttcctccatc tcttgctgca 1818
ttgctgctt gcaaaagtcc tcatgggctc gtggaaatg ctggaaatag ctatggat 1878
tcttgcatgt tctgagaagg ctatggAAC acaccacAGC aggatcgaag gttttatag 1938
agtctatTTT aaaatcacat ctggTatTTT cagcataaaa gaaatTTtag ttgtctttaa 1998
aatttgtatg agtgttaac ctttcttat tcatttgag gcttcttaaa gtggtagaat 2058
tccttccaaa ggcctcagat acatgttag ttcagtctt ccaacctcat ccttcctgc 2118
atcttagccc agttttacg aagaccctt aatcatgctt tnttaagagt ttttacccaa 2178
ctgcgttgga agacagaggt atccagactg attaataat tgaagaaaaaaa 2233

<210> 3
<211> 448
<212> PRT
<213> Mus musculus
<223> Clone mouse A55 derived from Day 13 mouse
embryonic heart

<400> 3
Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Trp
-20 -15 -10

Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp
-5 -1 1 5

Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
10 15 20 25

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
30 35 40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
45 50 55

Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
60 65 70

Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val
75 80 85

Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val
90 95 100 105

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
110 115 120

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
125 130 135

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
140 145 150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
155 160 165

Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val
170 175 180 185

Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
190 195 200

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
205 210 215

Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
220 225 230

Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser
235 240 245

Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
250 255 260 265

Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr
270 275 280

Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys
285 290 295

Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala
300 305 310

Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
315 320 325

Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
330 335 340 345

Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
350 355 360

Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
365 370 375

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile
380 385 390

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
395 400 405

Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
410 415 420 425

<210> 4
<211> 423
<212> PRT
<213> Mus musculus

<400> 4
Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
1 5 10 15

Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu

85

90

95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205

Pro Gly Tyr Glu Leu Glu Asp Gly Ile His Cys Ser Asp Met Asp
210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240

Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270

Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
275 280 285

Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu
290 295 300

Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala

340

345

350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
370 375 380

Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
385 390 395 400

Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
405 410 415

Tyr Val Ser Gln Tyr Pro Phe
420

<210> 5
<211> 1269
<212> DNA
<213> Mus musculus

<400> 5
cagtgcacaa acggcttga cctggaccgc cagtcaggac agtgtctaga tattgatgaa 60
tgccggacca tccctgaggc ttgtcgtgg gacatgtatgt gtgtcaacca gaatggcg 120
tatttgtca tccctcgaac caacccagtg tatcgaggc cttactcaaa tccctactct 180
acatcctact caggcccata cccagcagcg gcccaccag taccagctc caactacccc 240
acgatttcaa ggccttctgt ctgcccgtt gggatcaga tggatgaagg caaccagtgt 300
gtggatgtgg acgagtggtgc aacagactca caccagtgc accctaccca gatctgtatc 360
aacactgaag gaggttacac ctgctctgc accgatgggt actggcttct ggaagggcag 420
tgcctagata ttgatgaatg tcgctatgtt tactgccagc agctctgtgc aaatgttcca 480
ggatcctatt cctgtacatg caaccctgtt ttcacccctca acgacgttgc aaggcttgc 540
caagatgtga acgagtgcgaa aactgagaat ccctgtgttc agacctgtgt caacacctat 600
ggctcttca tctgccgctg tgacccagga tatgaacttg aggaagatgg cattcactgc 660
agtatgtatgg acgagtgcgag cttctccgag ttccctctgtc aacacgagtgt tggatgtttc 720
ccgggctcat acttctgctc gtgccctcca ggctacgtcc tggatgttgc taaccgaagc 780
tgccaggata tcaatgaatg tgagcaccga aaccacacgt gtacctact gcagacttgc 840
tacaatctac aagggggtt caaatgtatt gatcccatca gctgtgagga gccttatctg 900
ctgattggtg aaaaccgtt tatgtgtcct gctgagcaca ccagctgcag agaccagcca 960
ttcaccatcc tggatggta catggatgtg gtgtcaggac gctccgttcc tgctgacatc 1020
ttccagatgc aagcaacaac ccgataacctt ggtgcctatt acatttcca gatcaaatct 1080
ggcaacgagg gtcgagagtt ctatatgcgg caaacaggc ctatcagtgc caccctgg 1140
atgacacgccc ccatcaaagg gcctcgggac atccagctgg acttggagat gatcactgtc 1200
aacactgtca tcaacttcag aggcagctcc gtgatccgac tgccgatata tggatgtc 1260
tatccgttc 1269

<210> 6
<211> 1383
<212> DNA
<213> *Mus musculus*

<400> 6
atgggaccta gaagtttcga gccaatgcac agtggactct gcagacagag acgcatgata 60
ctcaactgtta ccatcttggc actctggctt ccacatcctg ggaatgcaca gcagcagtgc 120
acaacacggct ttgaccttggga ccggcagtca ggacagtgtc tagatattga tgaatgcccgg 180
accatccctg aggcttgcg tggggacatg atgtgtgtca accagaatgg cgggtatttg 240
tgcatccctc gaacccaaccc agtgtatcga gggccttact caaatcccta ctctacatcc 300
tactcaggcc catacccccgc agcggccccc ccagttaccag cttccaaacta ccccacgatt 360
tcaaggcctc ttgtctgccc ctttgggtat cagatggatg aaggcaacca gtgtgtggat 420
gtggacgagt gtgcaacaga ctcacaccag tgcaacccta cccagatctg tatcaacact 480
gaaggaggtt acacctgctc ctgcaccgat gggtaactggc ttctggaagg gcagtcgccta 540
gatattgatg aatgtcgcta tggtaactgc cagcagctct gtgcaaatgt tccaggatcc 600
tattcctgtta catgcaaccc tggtttccacc ctcaacgcacg atggaaggc ttgccaagat 660
gtgaacgagt gcgaaactga gaatccctgt gttcagacccgtgtcaacac ctagggctct 720
ttcatctgcc gctgtgaccc aggatatgaa cttgaggaag atggcattca ctgcagtgtat 780
atggacgagt gcaagttctc cgagttccctc tgtcaacacgc agtgtgtgaa ccagccgggc 840
tcatacttct gctcgtgccc tccaggctac gtcctgttgg atgataaccg aagctgcccag 900
gatataatg aatgtgagca ccgaaaccac acgtgtaccc cactgcacac ttgctacaat 960
ctacaagggg gcttcaaatttattgatccccatcagctgtg aggagcctta tctgctgatt 1020
ggtaaaaacc gctgtatgtg tccctgttag cacaccagct gcagagacca gccattcacc 1080
atccctgtatc gggacatgga tgggtgtca ggacgctccg ttcctgtga catcttccag 1140
atgcaagcaa caacccgata ccctggtgcc tattacattt tccagatcaa atctggcaac 1200
gagggtcgag agttctatatacgccaaaca gggcctatca gtgccaccct ggtgtatgaca 1260
cgccccatca aaggccctcg ggacatccag ctggacttgg agatgatcac tgtcaacact 1320
gtcatcaact tcagaggcag ctccgtgatc cgactgcggatataatgtgtc gcagttatccg 1380
ttc 1383

<210> 7
<211> 2429
<212> DNA
<213> *Mus musculus*

<220>
<223> Clone mouse A55b derived from Day 13 mouse
embryonic heart

<220>
<221> CDS
<222> (232)..(1614)

<220>
<221> sig_peptide
<222> (232) .. (339)

<220>
<221> mat_peptide
<222> (340)..(1614)

<400> 7
cagcatctcg agagaggcag cagacaacct ctctaggtca tttcttttc ttttgaaa 60
ggcagcaac gttgtgcga gtttataaaa tatcacacta catgtttttt aaatttggga 120
gactgctgac tacggcacca gcaattgctt tgctgcgacg gctgtgagac aagcagaagt 180
ctccgaacac ttctgtctgc gtttgcctca tgtgtgtat ttacagaggg a atg gga 237
Met Gly
-35
cct aga agt ttc gag cca atg cac agt gga ctc tgc aga cag aga cgc 285
Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln Arg Arg
-30 -25 -20
atg ata ctc act gtt acc atc ttg gca ctc tgg ctt cca cat cct ggg 333
Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His Pro Gly
-15 -10 -5
aat gca cag cag cag tgc aca aac ggc ttt gac ctg gac cgc cag tca 381
Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser
-1 1 5 10
gga cag tgt cta gat att gat gaa tgc cgg acc atc cct gag gct tgt 429
Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys
15 20 25 30
cgt ggg gac atg atg tgt gtc aac cag aat ggc ggg tat ttg tgc atc 477
Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile
35 40 45
cct cga acc aac cca gtg tat cga ggg cct tac tca aat ccc tac tct 525
Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser
50 55 60
aca tcc tac tca ggc cca tac cca gca gcg gcc cca cca gta cca gct 573
Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Pro Pro Val Pro Ala
65 70 75
tcc aac tac ccc acg att tca agg cct ctt gtc tgc cgc ttt ggg tat 621
Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr
80 85 90

cag atg gat gaa ggc aac cag tgc gat gtg gac gag tgc gca aca	669
Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr	
95 100 105 110	
gac tca cac cag tgc aac cct acc cag atc tgc aac act gaa gga	717
Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly	
115 120 125	
ggt tac acc tgc tcc tgc acc gat ggg tac tgg ctt ctg gaa ggg cag	765
Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln	
130 135 140	
tgc cta gat att gat gaa tgc tat ggt tac tgc cag cag ctc tgc	813
Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys	
145 150 155	
gca aat gtt cca gga tcc tat tcc tgc aca tgc aac cct ggt ttc acc	861
Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr	
160 165 170	
ctc aac gac gat gga agg tct tgc caa gat gtg aac gag tgc gaa act	909
Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr	
175 180 185 190	
gag aat ccc tgc gtt cag acc tgc aac acc tat ggc tct ttc atc	957
Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile	
195 200 205	
tgc cgc tgc gac cca gga tat gaa ctt gag gaa gat ggc att cac tgc	1005
Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Asp Gly Ile His Cys	
210 215 220	
agt gat atg gac gag tgc agc ttc tcc gag ttc ctc tgc caa cac gag	1053
Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu	
225 230 235	
tgc tgc aac cag ccg ggc tca tac ttc tgc tgc cct cca ggc tac	1101
Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr	
240 245 250	
gtc ctg ttg gat gat aac cga agc tgc cag gat atc aat gaa tgc gag	1149
Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu	
255 260 265 270	
cac cga aac cac acg tgc acc tca ctg cag act tgc tac aat cta caa	1197
His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln	
275 280 285	

ggg ggc ttc aaa tgt att gat ccc atc agc tgt gag gag cct tat ctg	1245		
Gly Gly Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu			
290	295	300	
ctg att ggt gaa aac cgc tgt atg tgt cct gct gag cac acc agc tgc	1293		
Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys			
305	310	315	
aga gac cag cca ttc acc atc ctg tat cgg gac atg gat gtg gtg tca	1341		
Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser			
320	325	330	
gga cgc tcc gtt cct gct gac atc ttc cag atg caa gca aca acc cga	1389		
Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg			
335	340	345	350
tac cct ggt gcc tat tac att ttc cag atc aaa tct ggc aac gag ggt	1437		
Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly			
355	360	365	
cga gag ttc tat atg cgg caa aca ggg cct atc agt gcc acc ctg gtg	1485		
Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val			
370	375	380	
atg aca cgc ccc atc aaa ggg cct cgg gac atc cag ctg gac ttg gag	1533		
Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu			
385	390	395	
atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc gtg atc	1581		
Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile			
400	405	410	
cga ctg cgg ata tat gtg tcg cag tat ccg ttc tgaggctctg gctaaggcct	1634		
Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe			
415	420	425	
ctgacactgc ctttcaccag caccgaggga cgggaggaga aaggaaacca gcaagaatga	1694		
gagcgagaca gacattgcac ctttcctgct gaatatctcc tgggggcatc agcctagcat	1754		
cttgaccat atctgtacta ttgcagatgg tcactctgaa ggacaccctg ccctcagttc	1814		
ctatgatgca gttatccaaa agtgttcatc tttagccctg atatgagggtt gccagtgact	1874		
cttcaaagcc ttccatttat ttccatcgtt ttataaaaaaa gaaaatagat tagatttgct	1934		
ggggatgag tcctcgaagg ttcaaaagac tgagtggctt gctctcacct cttcctctcc	1994		

ttcctccatc tcttgctgca ttgctgctt gcaaaaagtcc tcatgggctc gtgggaaatg 2054
ctggaaatag ctagttgct tcttgcatgt tctgagaagg ctatggaaac acaccacagc 2114
aggatcgaag gttttatag agtctatTTT aaaatcacat ctggTatttt cagcataaaa 2174
gaaatTTtag ttgtcttaa aatttgtatg agtgttaac ctttcttat tcattttgag 2234
gcttcTTaaa gtggtagaat tccttccaaa ggcctcagat acatgttatg ttcagtctt 2294
ccaacctcat ccttcctgc atcttagccc agttttacg aagaccctt aatcatgctt 2354
tnttaagagt ttttacccaa ctgcgttgg aagacagaggt atccagactg attaaataat 2414
tgaagaaaaa aaaaa 2429

<210> 8
<211> 461
<212> PRT
<213> Mus musculus
<223> Clone mouse A55b derived from Day 13 mouse
embryonic heart

<400> 8
Met Gly Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln
-35 -30 -25

Arg Arg Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His
-20 -15 -10 -5

Pro Gly Asn Ala Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg
-1 1 5 10

Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu
15 20 25

Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Tyr Leu
30 35 40

Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro
45 50 55 60

Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val
65 70 75

Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe
80 85 90

Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys
95 100 105

Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr
110 115 120

Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu
125 130 135 140

Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln
145 150 155

Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
160 165 170

Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys
175 180 185

Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser
190 195 200

Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Ile
205 210 215 220

His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln
225 230 235

His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro
240 245 250

Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu
255 260 265

Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn
270 275 280

Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro
285 290 295 300

Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr
305 310 315

Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val
320 325 330

Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr
335 340 345

Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn
350 355 360

Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr
365 370 375 380

Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp
385 390 395

Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser
400 405 410

Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
415 420 425

<210> 9
<211> 423
<212> PRT
<213> Mus musculus

<400> 9
Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
1 5 10 15

Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser
50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro
65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu
85 90 95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
145 150 155 160

Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
165 170 175

Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
180 185 190

Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205

Pro Gly Tyr Glu Leu Glu Asp Gly Ile His Cys Ser Asp Met Asp
210 215 220

Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240

Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
245 250 255

Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270

Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Phe Lys
275 280 285

Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu
290 295 300

Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
305 310 315 320

Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335

Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
340 345 350

Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
355 360 365

Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
370 375 380

Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
385 390 395 400

Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
405 410 415

Tyr Val Ser Gln Tyr Pro Phe
420

<210> 10
<211> 1269
<212> DNA
<213> Mus musculus

<400> 10
cagtgcacaa acggcttga cctggaccgc cagtcaggac agtgtctaga tattgatgaa 60
tgccggacca tccctgaggc ttgtcgtggg gacatgatgt gtgtcaacca gaatggcggg 120
tatttgtca tccctcgaac caacccagtg tatcgagggc cttactcaaa tccctactct 180
acatcctact caggcccata cccagcagcg gccccaccag taccagctc caactacccc 240
acgatttcaa ggcctttgt ctgcccgtt gggatcaga tggatgaagg caaccagtgt 300
gtggatgtgg acgagtggtgc aacagactca caccagtgc accctaccca gatctgtatc 360
aacactgaag gaggttacac ctgctcctgc accgatgggt actggcttct ggaaggcag 420
tgcctagata ttgatgaatg tcgctatggt tactgccagc agctctgtgc aaatgttcca 480
ggatcctatt cctgtacatg caacccttgtt ttcaccctca acgacgatgg aaggtcttgc 540
caagatgtga acgagtgcgaa aactgagaat ccctgtgttc agacctgtgt caacacctat 600
ggctcttca tctgccgtg tgacccagga tatgaacttg aggaagatgg cattcactgc 660
agtgatatgg acgagtgcgag cttctcccgag ttcacctgtc aacacgagtg tgtgaaccag 720
ccgggctcat acttctgtc gtgcctcga ggctacgtcc tggatgtga taaccgaagc 780
tgccaggata tcaatgaatg tgagcaccga aaccacacgt gtacctcaact gcagacttgc 840
tacaatctac aagggggctt caaatgtatt gatccatca gctgtgagga gccttatctg 900
ctgattgggtt aaaaccgtt tatgtgtcct gctgacaca ccagctgcag agaccagcca 960
ttcaccatcc tgtatcggtt catggatgtg gtgtcaggac gtcgttcc tgctgacatc 1020
ttccagatgc aagcaacaac ccgataccct ggtgcctatt acatccatca gatcaaatct 1080
ggcaacgagg gtcgagagtt ctatatgcgg caaacaggc ctatcgtgc caccctgggt 1140
atgacacgccc ccatcaaagg gcctcggtt acccagctgg acttggagat gatcactgtc 1200
aacactgtca tcaacttcag aggcagctcc gtgatccgac tgccgatata tgtgtcgcag 1260
tatccgttc 1269

<210> 11
<211> 1344
<212> DNA
<213> Homo sapiens

<400> 11
atgccaggaa taaaaaggat actcactgtt accattctgg ctctctgtct tccaaaggccct 60
ggaatgcac aggcacagtgc cacgaatggc tttgacctgg atgcgcgtc aggacagtgt 120

ttagatattg atgaatgccg aaccatcccc gaggcctgcc gaggagacat gatgtgtgtt 180
aaccaaaaatg gcgggtattt atgcattccc cggacaaacc ctgtgtatcg agggccctac 240
togaacccct actcgacccc ctactcaggt ccgtacccag cagctgccccc accactctca 300
gctccaaact atcccacgt ctccaggcct cttatatgcc gctttggata ccagatggat 360
gaaagcaacc aatgtgtgga tgtggacgag tgtgcaacag attcccacca gtgcaacccc 420
acccagatct gcatcaatac tgaaggcggg tacacctgct cctgcaccga cggatattgg 480
cttcttggaaag gccagtgcctt agacattgtat gaatgtcgct atggttactg ccagcagctc 540
tgtgcaatgtt ttccttggatc ctattcttgc acatgcaacc ctggttttac cctcaatggag 600
gatggaaaggctt ctgcaccaaga tgtgaacgag tgtgccaccg agaaccctg cgtcaaaacc 660
tgcgtcaaca cctacggctc tttcatctgc cgctgtgacc caggatatga acttgaggaa 720
gatggcgttc attgcagtga tatggacgag tgcaaccttct ctgagttcct ctgccaacat 780
gagtgtgtga accagcccg cacatacttc tgctcctgcc ctccaggcta catcctgctg 840
gatgacaacc gaagctgcca agacatcaac gaatgtgagc acaggaacca cacgtgcaac 900
ctgcagcaga cgtctacaa ttacaagggg ggcttcaaatt gcatcgaccc catccgctgt 960
gaggagcctt atctgaggat cagtgataac cgctgtatgt gtcctgctga gaaccctggc 1020
tgcagagacc agccctttac catcttgc acggacatgg acgtgggtgc aggacgctcc 1080
gttcccgctg acatcttcca aatgcaagcc acgacccgct accctggggc ctattacatt 1140
ttccagatca aatctggaa tgagggcaga gaattttaca tgccgcaaac gggccccatc 1200
agtgccaccc tggtgatgac acgccccatc aaagggccccc gggaaatcca gctggacttg 1260
gaaatgatca ctgtcaacac tgtcatcaac ttcagaggca gctccgtgat ccgactgcgg 1320
atatatgtgtc cgccgtaccc attc 1344

<210> 12
<211> 2328
<212> DNA
<213> Homo sapiens

<220>
<223> Clone human A55 derived from human brain

<220>
<221> CDS
<222> (169)..(1512)

<220>
<221> sig_peptide
<222> (169)..(237)

<220>
<221> mat_peptide
<222> (238)..(1512)

<400> 12
gaccggcgac tctcccggtc tcctctccac gactcgctcg gcccctctgg aataaaaacac 60
ccgcgagccc cgagggccca gaggaggccg acgtgcccga gctccctccgg gggtcccggc 120

Leu	Cys	Ala	Asn	Val	Pro	Gly	Ser	Tyr	Ser	Cys	Thr	Cys	Asn	Pro	Gly	
160					165						170					
ttt acc ctc aat gag gat gga agg tct tgc caa gat gtg aac gag tgt															801	
Phe	Thr	Leu	Asn	Glu	Asp	Gly	Arg	Ser	Cys	Gln	Asp	Val	Asn	Glu	Cys	
175					180					185						
gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct															849	
Ala	Thr	Glu	Asn	Pro	Cys	Val	Gln	Thr	Cys	Val	Asn	Thr	Tyr	Gly	Ser	
190					195				200							
ttc atc tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc gtt															897	
Phe	Ile	Cys	Arg	Cys	Asp	Pro	Gly	Tyr	Glu	Leu	Glu	Asp	Gly	Val		
205					210				215			220				
cat tgc agt gat atg gac gag tgc agc ttc tct gag ttc ctc tgc caa															945	
His	Cys	Ser	Asp	Met	Asp	Glu	Cys	Ser	Phe	Glu	Phe	Leu	Cys	Gln		
225					230				235							
cat gag tgt gtg aac cag ccc ggc aca tac ttc tgc tcc tgc cct cca															993	
His	Glu	Cys	Val	Asn	Gln	Pro	Gly	Thr	Tyr	Phe	Cys	Ser	Cys	Pro	Pro	
240					245				250							
ggc tac atc ctg ctg gat gac aac cga agc tgc caa gac atc aac gaa															1041	
Gly	Tyr	Ile	Leu	Leu	Asp	Asp	Asn	Arg	Ser	Cys	Gln	Asp	Ile	Asn	Glu	
255					260				265							
tgt gag cac agg aac cac acg tgc aac ctg cag cag acg tgc tac aat															1089	
Cys	Glu	His	Arg	Asn	His	Thr	Cys	Asn	Leu	Gln	Gln	Thr	Cys	Tyr	Asn	
270					275				280							
tta caa ggg ggc ttc aaa tgc atc gac ccc atc cgc tgt gag gag cct															1137	
Leu	Gln	Gly	Gly	Phe	Lys	Cys	Ile	Asp	Pro	Ile	Arg	Cys	Glu	Glu	Pro	
285					290				295			300				
tat ctg agg atc agt gat aac cgc tgt atg tgt cct gct gag aac cct															1185	
Tyr	Leu	Arg	Ile	Ser	Asp	Asn	Arg	Cys	Met	Cys	Pro	Ala	Glu	Asn	Pro	
305					310				315							
ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac atg gac gtg															1233	
Gly	Cys	Arg	Asp	Gln	Pro	Phe	Thr	Ile	Leu	Tyr	Arg	Asp	Met	Asp	Val	
320					325				330							
gtg tca gga cgc tcc gtt ccc gct gac atc ttc caa atg caa gcc acg															1281	
Val	Ser	Gly	Arg	Ser	Val	Pro	Ala	Asp	Ile	Phe	Gln	Met	Gln	Ala	Thr	
335					340				345							
acc cgc tac cct ggg gcc tat tac att ttc cag atc aaa tct ggg aat															1329	

Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn			
350	355	360	
gag ggc aga gaa ttt tac atg cgg caa acg ggc ccc atc agt gcc acc 1377			
Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr			
365	370	375	380
ctg gtg atg aca cgc ccc atc aaa ggg ccc cgg gaa atc cag ctg gac 1425			
Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp			
385	390	395	
ttg gaa atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc 1473			
Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser			
400	405	410	
gtg atc cga ctg cgg ata tat gtg tcg cag tac cca ttc tgagcctcg 1522			
Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe			
415	420	425	
gctggagcct ccgacgctgc ctctcattgg caccaaggga caggagaaga gagggaaataa 1582			
cagagagaat gagagcgaca cagacgttag gcatttcctg ctgaacgttt ccccgaaagag 1642			
tcagccccga cttcctgact ctcacctgta ctattgcaga cctgtcaccc tgcaggactt 1702			
gccaccccca gttcctatga tacagttatc aaaaagtatt atcattgctc ccctgataga 1762			
agattgttgg tgaattttca aggccttcag tttatttcca ctatttcaa agaaaataga 1822			
ttaggttgc ggggtctga gtctatgttc aaagactgtg aacagcttgc tgtcacttct 1882			
tcacctcttc cactccttct ctcactgtgt tactgctttg caaagacccg ggagctggcg 1942			
ggaaaccctg ggagtagcta gtttgcttt tgcgtacaca gagaaggcta tgtaaacaaa 2002			
ccacagcagg atcgaagggt ttttagagaa tgtgtttcaa aaccatgcct ggtattttca 2062			
accataaaag aagttcagt tgtccttaaa tttgtataac ggttaattc tgtcttgttc 2122			
attttagta ttttaaaaaa atatgtcgta gaattccttc gaaaggcctt cagacacatg 2182			
ctatgttctg tcttccaaa cccagtctcc tctccatttt agcccagtgt tttctttgag 2242			
gacccttaa tcttgcttc tttagaattt ttacccaatt ggattggaat gcagaggtct 2302			
ccaaactgat taaatattt aagaga			2328

<210> 13
 <211> 448
 <212> PRT
 <213> Homo sapiens
 <223> Clone human A55 derived from human brain

<400> 13
 Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
 -20 -15 -10
 Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
 -5 -1 1 5
 Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
 10 15 20 25
 Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
 30 35 40
 Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
 45 50 55
 Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
 60 65 70
 Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
 75 80 85
 Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
 90 95 100 105
 Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
 110 115 120
 Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
 125 130 135
 Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
 140 145 150
 Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
 155 160 165
 Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
 170 175 180 185
 Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
 190 195 200

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
205 210 215

Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
220 225 230

Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
235 240 245

Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
250 255 260 265

Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
270 275 280

Cys Tyr Asn Leu Gln Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
285 290 295

Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
300 305 310

Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
315 320 325

Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
330 335 340 345

Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
350 355 360

Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
365 370 375

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile
380 385 390

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
395 400 405

Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
410 415 420 425

<210> 14

<211> 423

<212> PRT

<213> Homo sapiens

<400> 14 Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu
5 10 15
1 Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met
20 25 30
Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn
35 40 45
Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser
50 55 60
Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro
65 70 75 80
Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu
85 90 95
Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110
Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Tyr Thr Cys
115 120 125
Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140
Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
145 150 155 160
Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp
165 170 175
Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys
180 185 190
Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205
Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val His Cys Ser Asp Met Asp
210 215 220
Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240

Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp
 245 250 255
 Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
 260 265 270
 Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
 275 280 285
 Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp
 290 295 300
 Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro
 305 310 315 320
 Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
 325 330 335
 Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
 340 345 350
 Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
 355 360 365
 Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
 370 375 380
 Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val
 385 390 395 400
 Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
 405 410 415
 Tyr Val Ser Gln Tyr Pro Phe
 420

<210> 15
 <211> 1269
 <212> DNA
 <213> Homo sapiens

<400> 15
 cagtgcacga atggcttga cctggatcgc cagtcaggac agtgtttaga tattgatgaa 60
 tgccgaacca tccccgaggc ctgcccagga gacatgatgt gtgttaacca aaatggcgaa 120
 tatttatgca ttccccggac aaaccctgtg tatcgagggc cctactcgaa cccctactcg 180
 accccctact caggtccgta cccagcagct gccccaccac tctcagctcc aaactatccc 240
 acgatctcca ggcctttat atgcccgttt ggataccaga tggatgaaag caaccaatgt 300

gtggatgtgg acgagtggtgc aacagattcc caccagtgc accccaccca gatctgcac 360
aatactgaag gcgggtacac ctgctcctgc accgacggat attggcttct ggaaggccag 420
tgcttagaca ttgatgaatg tcgctatgg tactgccagc agctctgtgc gaatgttcct 480
ggatcctatt cttgtacatg caaccctggt tttaccctca atgaggatgg aaggcttgc 540
caagatgtga acgagtggtgc caccgagaac ccctgcgtgc aaacctgcgt caacacctac 600
ggctcttc tctgccgtg tgacccagga tatgaacttg aggaagatgg cgttcattgc 660
agtgatatgg acgagtgca cttctctgag ttccctgc aacatgagtg tgtgaaccag 720
cccgacat acttctgctc ctgccctcca ggctacatcc tgctggatga caaccgaagc 780
tgccaagaca tcaacgaatg tgagcacagg aaccacacgt gcaacctgca gcagacgtgc 840
tacaatttac aagggggctt caaatgcattt gacccatcc gctgtgagga gccttatctg 900
aggatcgtg ataaccgctg tatgtgtcct gctgagaacc ctggctgcag agaccagccc 960
tttaccatct tgtacccggaa catggacgtg gtgtcaggac gctccgttcc cgctgacatc 1020
ttccaaatgc aagccacgac ccgctaccct ggggcctatt acatttcca gatcaaatct 1080
ggaaatgagg gcagagaatt ttacatgcgg caaacgggcc ccatcagtgc caccctggtg 1140
atgacacgcg ccataaagg gccccggaa atccagctgg acttggaaat gatcactgtc 1200
aacactgtca tcaacttcag aggcagctcc gtgatccgac tgccgatata tgtgtcgca 1260
tacccattc 1269

<210> 16
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16 35
cgattgaatt ctagacctgc ctgcgagnnnn nnnnn

<210> 17
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17 27
cgtttgca ctgctgctgt gcattcc

09/674379
534 Rec'd PCT/PTO 30 OCT 2000

SEQUENCE LISTING

<110> Ono Pharmaceutical Co., Ltd.

<120> Novel polypeptides, cDNA coding these polypeptides and Use thereof

<130> ONF-2970PCT

<141> 1999-04-28

<150> JP 10-119731

<151> 1998-04-28

<160> 17

<170> PatentIn Ver. 2.0

<210> 1

<211> 448

<212> PRT

<213> *Mus musculus*

<400> 1

Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Trp

-23 -20 -15 -10

Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp

-5 1 5

Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
10 15 20 25

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
30 35 40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
45 50 55

Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
60 65 70

Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val
75 80 85

Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val
90 95 100 105

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
110 115 120

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
125 130 135

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
140 145 150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys
155 160 165

Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val
170 175 180 185

Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
190 195 200

Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
205 210 215

Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
220 225 230
Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser
235 240 245
Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
250 255 260 265
Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr
270 275 280
Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys
285 290 295
Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala
300 305 310
Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
315 320 325
Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
330 335 340 345
Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
350 355 360
Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile
365 370 375
Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile
380 385 390
Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg
395 400 405
Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
410 415 420 425

<210> 2

<211> 1344

<212> DNA

<213> *Mus musculus*

<400> 2

atgccaggat taaaaaggat actcaactgtt accatcttgg cactctggct tccacatcct 60
gggaatgcac agcagcagtg cacaaacggc tttgacctgg accgccagtc aggacagtgt 120
ctagatattg atgaatgcgc gaccatccct gaggcttgcgt gtggggacat gatgtgtgtc 180
aaccagaatg gcgggtattt gtgcattccct cgaaccaacc cagtgtatcg agggccttac 240
tcaaataccct actctacatc ctactcaggc ccataccag cagcggccccc accagtagcca 300
gcttccaact accccacgat ttcaaggcct cttgtctgcc gctttggta tcagatggat 360
gaaggcaacc agtgtgtgga tgtggacgag tgtgcaacag actcacacca gtgcaaccct 420
acccagatct gtatcaacac tgaaggaggt tacacctgct cctgcaccga tgggtactgg 480
.cttctggaag ggcagtgcct agatattgtt gaatgtcgct atggttactg ccagcagctc 540
tgtgcaaatg ttccaggatc ctattcctgt acatgcaacc ctggtttcac cctcaacgac 600
gatggaaggt cttgccaaga tgtgaaacgag tgcgaaactg agaatccctg tggcagacc 660
tgtgtcaaca cctatggctc tttcatctgc cgctgtgacc caggatatga acttgaggaa 720
gatggcattc actgcagtga tatggacgag tgcagcttct ccgagttcct ctgtcaacac 780
gagtgtgtga accagccggg ctcatacttc tgctcgtgcc ctccaggcta cgtcctgtt 840
gatgataacc gaagctgcca ggtatcaat gaatgtgagc accgaaacca cacgtgtacc 900
tcactgcaga cttgctacaa tctacaaggg ggcttcaaattt gtattgtatcc catcagctgt 960
gaggagcctt atctgctgat tggtaaaaac cgctgtatgt gtcctgctga gcacaccagc 1020
tgcagagacc agccattcac catcctgtat cgggacatgg atgtgggtgc aggacgctcc 1080

gttcctgctg acatcttcca gatgcaagca acaacccgat accctggtgc ctattacatt 1140
ttccagatca aatctggcaa cgagggtcga gagttctata tgccgcaaac agggcctatc 1200
agtgcaccc tggtgatgac acgccccatc aaagggcctc gggacatcca gctggacttg 1260
gagatgatca ctgtcaacac tgtcatcaac ttcagaggca gctccgtgat ccgactgcgg 1320
atatatgtgt cgcaagtatcc gttc 1344

<210> 3

<211> 2233

<212> DNA

<213> *Mus musculus*

<220>

<223> Clone mouse A55 derived from Day 13 mouse embryonic heart

<220>

<221> CDS

<222> (75)..(1418)

<220>

<221> sig_peptide

<222> (75)..(143)

<220>

<221> mat_peptide

<222> (144)..(1418)

<400> 3

aattcggcac gagccccagt cccaccgcag agcctgcctt cctcgcgctcg cttctccctcc 60
cgcgcatctt ggat atg cca gga tta aaa agg ata ctc act gtt acc atc 110
Met Pro Gly Leu Lys Arg Ile Leu Thr Val Thr Ile
-20 -15
ttg gca ctc tgg ctt cca cat cct ggg aat gca cag cag cag tgc aca 158
Leu Ala Leu Trp Leu Pro His Pro Gly Asn Ala Gln Gln Gln Cys Thr
-10 -5 -1 1 5
aac ggc ttt gac ctg gac cgc cag tca gga cag tgt cta gat att gat 206
Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp
10 15 20
gaa tgc cgg acc atc cct gag gct tgt cgt ggg gac atg atg tgt gtc 254
Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val
25 30 35
aac cag aat ggc ggg tat ttg tgc atc cct cga acc aac cca gtg tat 302
Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr
40 45 50
cga ggg cct tac tca aat ccc tac tct aca tcc tac tca ggc cca tac 350
Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr
55 60 65
cca gca gcg gcc cca cca gta cca gct tcc aac tac ccc acg att tca 398
Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro Thr Ile Ser
70 75 80 85
agg cct ctt gtc tgc cgc ttt ggg tat cag atg gat gaa ggc aac cag 446
Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu Gly Asn Gln

90 95 100
tgt gtg gat gtg gac gag tgt gca aca gac tca cac cag tgc aac cct 494
Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro
105 110 115
acc cag atc tgt atc aac act gaa gga ggt tac acc tgc tcc tgc ac~~t~~ 542
Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr
120 125 130
gat ggg tac tgg ctt ctg gaa ggg cag tgc cta gat att gat gaa tgt 590
Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys
135 140 145
cgc tat ggt tac tgc cag cag ctc tgt gca aat gtt cca gga tcc tat 638
Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr
150 155 160 165
tcc tgt aca tgc aac cct ggt ttc acc ctc aac gac gat gga agg tct 686
Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp Gly Arg Ser
170 175 180
tgc caa gat gtg aac gag tgc gaa act gag aat ccc tgt gtt cag acc 734
Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys Val Gln Thr
185 190 195
tgt gtc aac acc tat ggc tct ttc atc tgc cgc tgt gac cca gga tat 782
Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr
200 205 210
gaa ctt gag gaa gat ggc att cac tgc agt gat atg gac gag tgc agc 830
Glu Leu Glu Glu Asp Gly Ile His Cys Ser Asp Met Asp Glu Cys Ser
215 220 225
ttc tcc gag ttc ctc tgt caa cac gag tgt gtg aac cag ccg ggc tca 878

Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Ser
230 235 240 245
tac ttc tgc tcg tgc cct cca ggc tac gtc ctg ttg gat gat aac cga 926
Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp Asp Asn Arg
250 255 260
agc tgc cag gat atc aat gaa tgt gag cac cga aac cac acg tgt acc 974
Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Thr
265 270 275
tca ctg cag act tgc tac aat cta caa ggg ggc ttc aaa tgt att gat 1022
Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp
280 285 290
ccc atc agc tgt gag gag cct tat ctg ctg att ggt gaa aac aac cgc tgt 1070
Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu Asn Arg Cys
295 300 305
atg tgt cct gct gag cac acc agc tgc aga gac cag cca ttc acc atc 1118
Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro Phe Thr Ile
310 315 320 325
ctg tat cgg gac atg gat gtg gtg tca gga cgc tcc gtt cct gct gac 1166
Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp
330 335 340
atc ttc cag atg caa gca aca acc cga tac cct ggt gcc tat tac att 1214
Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile
345 350 355
ttc cag atc aaa tct ggc aac gag ggt cga gag ttc tat atg cgg caa 1262
Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln
360 365 370

aca ggg cct atc agt gcc acc ctg gtg atg aca cgc ccc atc aaa ggg 1310
Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly
375 380 385
cct cgg gac atc cag ctg gac ttg gag atg atc act gtc aac act gtc 1358
Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val
390 395 400 405
atc aac ttc aga ggc agc tcc gtg atc cga ctg cgg ata tat gtg tcg 1406
Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser
410 415 420
cag tat ccg ttc tgagcctctg gctaaggcct ctgacactgc ctttcaccag 1458
Gln Tyr Pro Phe
425
caccgaggga cgggaggaga aaggaaacca gcaagaatga gagcgagaca gacattgcac 1518
ctttcctgct gaatatctcc tggggcattc agcctagcat cttgacccat atctgtacta 1578
ttgcagatgg tcactctgaa ggacaccctg ccctcagttc ctatgtgca gttatccaaa 1638
agtgttcatc ttagcccctg atatgaggtt gccagtgact cttcaaagcc ttccatttat 1698
ttccatcggtt ttataaaaaaa gaaaatagat tagatttgct gggtatgag tcctcgaagg 1758
ttcaaaagac tgagtggctt gcttcaccc tttcctctcc ttcctccatc tcttgctgca 1818
ttgctgcttt gcaaaagtcc tcatggcctc gtggaaatg ctggaaatag ctagtttgct 1878
tcttgatgt tctgagaagg ctatggAAC acaccacAGC aggatcGAAG gttttatAG 1938
agtctatTTT aaaatcacat ctggTatTTT cAGcataAAA gaaATTTAG ttgtcttAA 1998
aatttgatg agtgttaac ctTTTCTTAT tcattttAG gcttcttAA gtggtagAA 2058
tccttccAAA ggcctcAGat acatgttATG ttcaGtctt ccaacctcat ctttcctgc 2118
atcttagccc agTTTTACG aAGACCCttt aatcatgctt tnttaAGAGt tttacccAA 2178
ctgcgttggA agacagAGGT atccAGACTG attaaATAAAt tgaAGAAAAA aaaaa 2233

<210> 4

<211> 423

<212> PRT

<213> *Mus musculus*

<400> 4

Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu

1 5 10 15

Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met

20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn

35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser

50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro

65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu

85 90 95

Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln

100 105 110

Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys

115 120 125

Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile

130 135 140

Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro

145 150 155 160
Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
165 170 175
Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
180 185 190
Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205
Pro Gly Tyr Glu Leu Glu Asp Gly Ile His Cys Ser Asp Met Asp
210 215 220
Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240
Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
245 250 255
Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270
Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Phe Lys
275 280 285
Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu
290 295 300
Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
305 310 315 320
Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335
Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
340 345 350
Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr

355	360	365	
Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro			
370	375	380	
Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val			
385	390	395	400
Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile			
405	410	415	
Tyr Val Ser Gln Tyr Pro Phe			
420			

210 5

211 1269

<212> DNA

<213> *Mus musculus*

<400> 5

cagtgcacaa acggcttga cctggaccgc cagtcaggac agtgtctaga tattgatgaa 60
tgccggacca tccctgaggc ttgtcgtgg gacatgatgt gtgtcaacca gaatggcggg 120
tatttgta cccctcgaaac caacccagtg tatcgagggc cttactcaaa tccctactct 180
acatcctact caggcccata cccagcagcg gccccaccag taccagctc caactacccc 240
acgatttcaa ggcctttgt ctgcccgtt gggtatcaga tggatgaagg caaccagtgt 300
gtggatgtgg acgagtggtgc aacagactca caccagtgca accctaccca gatctgtatc 360
aacactgaag gaggttacac ctgctcctgc accgatgggt actggcttct ggaagggcag 420
tgcctagata ttgatgaatg tcgctatggt tactgccagc agctctgtgc aaatgttcca 480
ggatcctatt cctgtacatg caaccctggt ttcaccctca acgacgatgg aaggtcttgc 540

caagatgtga acgagtgcga aactgagaat ccctgtgttc agacctgtgt caacacctat 600
ggctcttca tctgccgctg tgacccagga tatgaacttg aggaagatgg cattcactgc 660
agtgatatgg acgagtgcag cttctccgag ttcctctgtc aacacgagtg tgtgaaccag 720
ccgggctcat acttctgctc gtgccctcca ggctacgtcc tggatga taaccgaagc 780
tgccaggata tcaatgaatg tgagcaccga aaccacacgt gtacctcaact gcagacttgc 840
tacaatctac aagggggcatt caaatgtatt gatcccatca gctgtgagga gccttatctg 900
ctgattggtg aaaaccgctg tatgtgtcct gctgagcaca ccagctgcag agaccagcca 960
ttcaccatcc tgtatcgga catggatgtg gtgtcaggac gctccgttcc tgctgacatc 1020
ttccagatgc aagcaacaac ccgataccct ggtgcctatt acatcccata gatcaaatct 1080
ggcaacgagg gtcgagagtt ctatatgcgg caaacaggc ctatcagtgc caccctgg 1140
atgacacgccc ccatcaaagg gcctcggac atccagctgg acttggagat gatcaactgtc 1200
aacactgtca tcaacttcag aggcagctcc gtgatccgac tgccgatata tgtgtcgcag 1260
tatccgttc 1269

<210> 6

<211> 461

<212> PRT

<213> *Mus musculus*

<400> 6

Met Gly Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln

-35 -30 -25

Arg Arg Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His

-20 -15 -10 -5

Pro Gly Asn Ala Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg

59874379.012302

-1 1 5 10

Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu
15 20 25

Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu
30 35 40

Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro
45 50 55 60

Tyr Ser Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val
65 70 75

Pro Ala Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe
80 85 90

Gly Tyr Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys
95 100 105

Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr
110 115 120

Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu
125 130 135 140

Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln
145 150 155

Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
160 165 170

Phe Thr Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys
175 180 185

Glu Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser
190 195 200

Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Asp Gly Ile

205 210 215 220
His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln
225 230 235
His Glu Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro
240 245 250
Gly Tyr Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu
255 260 265
Cys Glu His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn
270 275 280
Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro
285 290 295 300
Tyr Leu Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr
305 310 315
Ser Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val
320 325 330
Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr
335 340 345
Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn
350 355 360
Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr
365 370 375 380
Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp
385 390 395
Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser
400 405 410
Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe

415

420

425

<210> 7

<211> 1383

<212> DNA

<213> *Mus musculus*

<400> 7

atgggaccta gaagttcga gccaatgcac agtggactct gcagacagag acgcatgata 60
ctcaactgtta ccatcttggc actctggctt ccacatcctg ggaatgcaca gcagcagtgc 120
acaaacggct ttgacctgga ccgcccagtca ggacagtgtc tagatattga tgaatgccgg 180
accatccctg aggcttgcg tggggacatg atgtgtgtca accagaatgg cgggtatttg 240
tgcatccctc gaaccaaccc agtgtatcga gggccttact caaatcccta ctctacatcc 300
tactcaggcc catacccagc agcggcccca ccagtaccag cttccaacta ccccacgatt 360
tcaaggcctc ttgtctgccg ctggggat cagatggatg aaggcaacca gtgtgtggat 420
gtggacgagt gtgcaacaga ctcacaccag tgcaacccta cccagatctg tatcaacact 480
gaaggagggtt acacctgctc ctgcaccgat gggtaactggc ttctggaagg gcagtgcccta 540
gatattgatg aatgtcgcta tggttactgc cagcagctct gtgcaaatgt tccaggatcc 600
tattcctgta catgcaaccc tggtttacc ctcaacgacg atggaaggta ttgccaagat 660
gtgaacgagt gcgaaactga gaatccctgt gttcagacac gttcaacac cttatggctct 720
ttcatctgcc gctgtgaccc aggatatgaa cttgaggaag atggcattca ctgcagtgtat 780
atggacgagt gcagcttctc cgagttccctc tgtcaacacg agtgtgtgaa ccagccggc 840
tcatacttct gctcgtgcc tccaggctac gtcctgttgg atgataaccg aagctgccag 900
gatataatg aatgtgagca ccgaaaccac acgtgtaccc cactgcagac ttgctacaat 960
ctacaagggg gcttcaaatg tattgatccc atcagctgtg aggagcccta tctgctgatt 1020

ggtgaaaacc gctgtatgtc tcctgctgag cacaccagct gcagagacca gccattcacc 1080
atcctgtatc gggacatgga tgtggtgtca ggacgctccg ttcctgctga catcttccag 1140
atgcaagcaa caacccgata ccctggtgcc tattacattt tccagatcaa atctggcaac 1200
gaggggtcgag agttctatat gcggcaaaca gggcctatca gtgccaccct ggtgatgaca 1260
cgccccatca aagggcctcg ggacatccag ctggacttgg agatgatcac tgtcaacact 1320
gtcatcaact tcagaggcag ctccgtgatc cgactgcgga tatatgtgtc gcagtatccg 1380
ttc 1383

<210> 8

<211> 2429

<212> DNA

<213> *Mus musculus*

<220>

<223> Clone mouse A55b derived from Day 13 mouse embryonic heart

<220>

<221> CDS

<222> (232)..(1614)

<220>

<221> sig_peptide

<222> (232)..(339)

<220>

<221> mat_peptide

<222> (340)..(1614)

<400> 8

cagcatctcg agagaggcag cagacaacct ctctaggta tttcttttc tttttggaaa 60
ggcagcaac gttgtgcga gtttataaaa tatcacacta catgttttt aaatttggaa 120
gactgctgac tacggcacca gcaattgctt tgctgcgacg gctgtgagac aagcagaagt 180
ctccgaacac ttctgtctgc gtttgctcta tgtgtgtgat ttacagaggg a atg gga 237

Met Gly

-35

cct aga agt ttc gag cca atg cac agt gga ctc tgc aga cag aga cgc 285

Pro Arg Ser Phe Glu Pro Met His Ser Gly Leu Cys Arg Gln Arg Arg

-30

-25

-20

atg ata ctc act gtt acc atc ttg gca ctc tgg ctt cca cat cct ggg 333

Met Ile Leu Thr Val Thr Ile Leu Ala Leu Trp Leu Pro His Pro Gly

-15

-10

-5

aat gca cag cag cag tgc aca aac ggc ttt gac ctg gac cgc cag tca 381

Asn Ala Gln Gln Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser

-1 1

5

10

gga cag tgt cta gat att gat gaa tgc cgg acc atc cct gag gct tgt 429

Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys

15

20

25

30

cgt ggg gac atg atg tgt gtc aac cag aat ggc ggg tat ttg tgc atc 477

Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile

35

40

45

cct cga acc aac cca gtg tat cga ggg cct tac tca aat ccc tac tct 525

Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser
 50 55 60
 aca tcc tac tca ggc cca tac cca gca gcg gcc cca cca gta cca gct 573
 Thr Ser Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala
 65 70 75
 tcc aac tac ccc acg att tca agg cct ctt gtc tgc cgc ttt ggg tat 621
 Ser Asn Tyr Pro Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr
 80 85 90
 cag atg gat gaa ggc aac cag tgt gtg gat gtg gac gag tgt gca aca 669
 Gln Met Asp Glu Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr
 95 100 105 110
 gac tca cac cag tgc aac cct acc cag atc tgt atc aac act gaa gga 717
 Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly
 115 120 125
 ggt tac acc tgc tcc tgc acc gat ggg tac tgg ctt ctg gaa ggg cag 765
 Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln
 130 135 140
 tgc cta gat att gat gaa tgt cgc tat ggt tac tgc cag cag ctc tgt 813
 Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys
 145 150 155
 gca aat gtt cca gga tcc tat tcc tgt aca tgc aac cct ggt ttc acc 861
 Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr
 160 165 170
 ctc aac gac gat gga agg tct tgc caa gat gtg aac gag tgc gaa act 909
 Leu Asn Asp Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr
 175 180 185 190

gag aat ccc tgt gtt cag acc tgt gtc aac acc tat ggc tct ttc atc 957
Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile
195 200 205
tgt gac cca gga tat gaa ctt gag gaa gat ggc att cac tgc 1005
Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Asp Gly Ile His Cys
210 215 220
agt gat atg gac gag tgc agc ttc tcc gag ttc ctc tgt caa cac gag 1053
Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu
225 230 235
tgt gtg aac cag ccg ggc tca tac ttc tgc tcg tgc cct cca ggc tac 1101
Cys Val Asn Gln Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr
240 245 250
gtc ctg ttg gat gat aac cga agc tgc cag gat atc aat gaa tgt gag 1149
Val Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu
255 260 265 270
cac cga aac cac acg tgt acc tca ctg cag act tgc tac aat cta caa 1197
His Arg Asn His Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln
275 280 285
ggg ggc ttc aaa tgt att gat ccc atc agc tgt gag gag cct tat ctg 1245
Gly Gly Phe Lys Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu
290 295 300
ctg att ggt gaa aac cgc tgt atg tgt cct gct gag cac acc agc tgc 1293
Leu Ile Gly Glu Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys
305 310 315
aga gac cag cca ttc acc atc ctg tat cgg gac atg gat gtg gtg tca 1341
Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser

320 325 330
gga cgc tcc gtt cct gct gac atc ttc cag atg caa gca aca acc cga 1389
Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg
335 340 345 350
tac cct ggt gcc tat tac att ttc cag atc aaa tct ggc aac gag ggt 1437
Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly
355 360 365
cga gag ttc tat atg cgg caa aca ggg cct atc agt gcc acc ctg gtg 1485
Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val
370 375 380
atg aca cgc ccc atc aaa ggg cct cgg gac atc cag ctg gac ttg gag 1533
Met Thr Arg Pro Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu
385 390 395
atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc gtg atc 1581
Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile
400 405 410
cga ctg cgg ata tat gtg tcg cag tat ccg ttc tgaggctctg gctaaggcct 1634
Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
415 420 425
ctgacactgc ctttcaccag caccgaggga cgggaggaga aaggaaacca gcaagaatga 1694
gagcgagaca gacattgcac ctttcctgct gaatatctcc tggggcatac agcctagcat 1754
cttgaccat atctgtacta ttgcagatgg tcactctgaa ggacaccctg ccctcagttc 1814
ctatgatgca gttatccaaa agtgttcatac ttagccctg atatgagggtt gccagtgact 1874
cttcaaagcc ttccatattt ttccatcggtt ttataaaaaa gaaaatagat tagatttgct 1934
ggggatgatgag tcctcgaagg ttcaaaagac tgagtggctt gctctcacct cttcctctcc 1994
ttcctccatc ttttgctgca ttgctgcttt gcaaaagtcc tcatggcgtc gtggaaatg 2054

ctggaaatag ctagtttgc tcttgcatgt tctgagaagg ctatggaaac acaccacagc 2114
aggatcgaag gttttatag agtctatTTT aaaatcacat ctggtatttt cagcataaaa 2174
gaaattttag ttgtcttaa aatttgtatg agtgttaac ctttcttat tcattttgag 2234
gcttcttaaa gtggtagaat tccttccaaa ggcctcagat acatgttatg ttcagtctt 2294
ccaacctcat ccttcctgc atcttagccc agttttacg aagaccctt aatcatgctt 2354
tnttaagagt ttttacccaa ctgcgttgaa agacagaggt atccagactg attaaataat 2414
tgaagaaaaa aaaaaa 2429

<210> 9

<211> 423

<212> PRT

<213> *Mus musculus*

<400> 9

Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu

1 5 10 15

Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met

20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn

35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Ser Tyr Ser

50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Val Pro Ala Ser Asn Tyr Pro

65 70 75 80

Thr Ile Ser Arg Pro Leu Val Cys Arg Phe Gly Tyr Gln Met Asp Glu

85 90 95
Gly Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110
Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125
Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140
Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
145 150 155 160
Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Asp Asp
165 170 175
Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Glu Thr Glu Asn Pro Cys
180 185 190
Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205
Pro Gly Tyr Glu Leu Glu Asp Gly Ile His Cys Ser Asp Met Asp
210 215 220
Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240
Pro Gly Ser Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Val Leu Leu Asp
245 250 255
Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270
Thr Cys Thr Ser Leu Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
275 280 285
Cys Ile Asp Pro Ile Ser Cys Glu Glu Pro Tyr Leu Leu Ile Gly Glu

290 295 300
Asn Arg Cys Met Cys Pro Ala Glu His Thr Ser Cys Arg Asp Gln Pro
305 310 315 320
Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335
Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
340 345 350
Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
355 360 365
Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
370 375 380
Ile Lys Gly Pro Arg Asp Ile Gln Leu Asp Leu Glu Met Ile Thr Val
385 390 395 400
Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
405 410 415
Tyr Val Ser Gln Tyr Pro Phe
420

<210> 10

<211> 1269

<212> DNA

<213> *Mus musculus*

<400> 10

cagtgcacaa acggcttga cctggaccgc cagtcaggac agtgtctaga tattgatgaa 60

tgccggacca tccctgaggc ttgtcgtgg gacatgatgt gtgtcaacca gaatggcggg 120
tatttgtca tccctcgaac caacccagtg tatcgagggc cttactcaaa tccctactct 180
acatcctact caggcccata cccagcagcg gccccaccag taccagcttc caactacccc 240
acgatttcaa ggcctttgt ctggcgctt gggtatcaga tggatgaagg caaccagtgt 300
gtggatgtgg acgagtgtgc aacagactca caccagtca accctaccca gatctgtatc 360
aacactgaag gaggttacac ctgctcctgc accgatgggt actggcttct ggaagggcag 420
tgcctagata ttgatgaatg tcgctatggt tactgccagc agctctgtgc aaatttcca 480
ggatcctatt cctgtacatg caaccctggt ttcaccctca acgacgatgg aaggcttgc 540
caagatgtga acgagtgcga aactgagaat ccctgtgttc agacctgtgt caacacctat 600
ggctcttca tctggcgctg tgacccagga tatgaacttg aggaagatgg cattcactgc 660
agtgatatgg acgagtgcag cttctccgag ttcctctgtc aacacgatgg tgtgaaccag 720
ccgggctcat acttctgctc gtgccctcca ggctacgtcc tggatga taaccgaagc 780
tgccaggata tcaatgaatg tgagcaccga aaccacacgt gtacctcaact gcagacttgc 840
tacaatctac aagggggctt caaatgtatt gatcccatca gctgtgagga gccttatctg 900
ctgattggtg aaaaccgctg tatgtgcct gctgagcaca ccagctgcag agaccagcca 960
ttcaccatcc tgtatcgga catggatgtg gtgtcaggac gctccgttcc tgctgacatc 1020
ttccagatgc aagcaacaac ccgataccct ggtgcctatt acatcccata gatcaaatct 1080
ggcaacgagg gtcgagagtt ctatatgcgg caaacagggc ctatcgtgc caccctggtg 1140
atgacacgcc ccatcaaagg gcctcgac atccagctgg acttggagat gatcactgtc 1200
aacactgtca tcaacttcag aggtagtcc gtgatccgac tgccgatata tgtgtgcag 1260
tatccgttc 1269

<210> 11

<211> 448

<212> PRT

<213> Homo sapiens

<400> 11

Met Pro Gly Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys
-20 -15 -10

Leu Pro Ser Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp
-5 -1 1 5

Leu Asp Arg Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr
10 15 20 25

Ile Pro Glu Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly
30 35 40

Gly Tyr Leu Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr
45 50 55

Ser Asn Pro Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala
60 65 70

Pro Pro Leu Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile
75 80 85

Cys Arg Phe Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val
90 95 100 105

Asp Glu Cys Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys
110 115 120

Ile Asn Thr Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp
125 130 135

Leu Leu Glu Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr
140 145 150

Cys Gln Gln Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys

155 160 165
Asn Pro Gly Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val
170 175 180 185
Asn Glu Cys Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr
190 195 200
Tyr Gly Ser Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu
205 210 215
Asp Gly Val His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe
220 225 230
Leu Cys Gln His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser
235 240 245
Cys Pro Pro Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp
250 255 260 265
Ile Asn Glu Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr
270 275 280
Cys Tyr Asn Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys
285 290 295
Glu Glu Pro Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala
300 305 310
Glu Asn Pro Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp
315 320 325
Met Asp Val Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met
330 335 340 345
Gln Ala Thr Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys
350 355 360
Ser Gly Asn Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile

365

370

375

Ser Ala Thr Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile

380

385

390

Gln Leu Asp Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg

395

400

405

Gly Ser Ser Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe

410

415

420

425

<210> 12

<211> 1344

<212> DNA

<213> Homo sapiens

<400> 12

atgccaggaa taaaaaggat actcaactgtt accattctgg ctctctgtct tccaaaggcct 60
gggaatgcac aggcacagtg cacgaatggc tttgacacctgg atcgccagtc aggacagtgt 120
ttagatattg atgaatgcgcg aaccatcccc gaggcctgcc gaggagacat gatgtgtgtt 180
aaccaaaatg gcgggtatatt atgcattccc cggacaaacc ctgtgtatcg agggccctac 240
tcgaaccctt actcgacccc ctactcaggt ccgtacccag cagctgccccc accactctca 300
gctccaaact atcccacgat ctccaggcct cttatatgcc gctttggata ccagatggat 360
gaaagcaacc aatgtgtgga tgtggacgag tgtgcaacag attcccacca gtgcaacccc 420
acccagatct gcatcaatac tgaaggcggg tacacctgct cctgcaccga cggatattgg 480
cttctggaag gccagtgcctt agacattgat gaatgtcgct atggttactg ccagcagctc 540
tgtgcaatg ttcctggatc ctattcttgt acatgcaacc ctggtttac cctcaatgag 600
gatgaaaggctt gccaaga tgtgaacgag tgtgccaccc agaaccctg cgtgcaaacc 660

tgcgtcaaca cctacggctc tttcatctgc cgctgtgacc caggatatga acttgaggaa 720
gatggcggttc attgcagtga tatggacgag tgcagcttct ctgagttcct ctgccaacat 780
gagtgtgtga accagccgg cacatacttc tgctcctgcc ctccaggcta catcctgctg 840
gatgacaacc gaagctgcca agacatcaac gaatgtgagc acaggaacca cacgtgcaac 900
ctgcagcaga cgtgctacaa tttacaaggg ggcttcaaatt gcatcgaccc catccgctgt 960
gaggagcctt atctgaggat cagtgataac cgctgtatgt gtcctgctga gaaccctggc 1020
tgcagagacc agccctttac catcttgtac cgggacatgg acgtgggtgc aggacgctcc 1080
gttcccgctg acatcttcca aatgcaagcc acgacccgct accctggggc ctattacatt 1140
ttccagatca aatctggaa tgagggcaga gaattttaca tgccgaaac gggccccatc 1200
agtgccaccc tggtgatgac acgccccatc aaagggcccc gggaaatcca gctggacttg 1260
gaaatgatca ctgtcaacac tgtcatcaac ttcagaggca gctccgtgat ccgactgcgg 1320
atatatgtgt cgcatgtaccc attc 1344

<210> 13

<211> 2328

<212> DNA

<213> Homo sapiens

<220>

<223> Clone human A55 derived from human brain

<220>

<221> CDS

<222> (169)..(1512)

<220>

<221> sig_peptide

<222> (169)..(237)

<220>

<221> mat_peptide

<222> (238)..(1512)

<400> 13

gaccggcgc tctccccgtg tcctctccac gactcgctcg gccctctgg aataaaacac 60
ccgcgagccc cgagggccca gagggaggccg acgtgcccga gctcctccgg gggtcccgcc 120
cgcgagcttt cttctcgccct tcgcacatctcc tcctcgcgcg tcttggac atg cca gga 177

Met Pro Gly

-23

ata aaa agg ata ctc act gtt acc att ctg gct ctc tgt ctt cca agc 225

Ile Lys Arg Ile Leu Thr Val Thr Ile Leu Ala Leu Cys Leu Pro Ser

-20 -15 -10 -5

cct ggg aat gca cag gca cag tgc acg aat ggc ttt gac ctg gat cgc 273

Pro Gly Asn Ala Gln Ala Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg

-1 1 5 10

cag tca gga cag tgt tta gat att gat gaa tgc cga acc atc ccc gag 321

Gln Ser Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu

15 20 25

gcc tgc cga gga gac atg atg tgt gtt aac caa aat ggc ggg tat tta 369

Ala Cys Arg Gly Asp Met Met Cys Val Asn Gln Asn Gly Gly Tyr Leu

30 35 40

tgc att ccc cgg aca aac cct gtg tat cga ggg ccc tac tcg aac ccc 417
Cys Ile Pro Arg Thr Asn Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro
45 50 55 60
tac tcg acc ccc tac tca ggt ccg tac cca gca gct gcc cca cca ctc 465
Tyr Ser Thr Pro Tyr Ser Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu
65 70 75
tca gct cca aac tat ccc acg atc tcc agg cct ctt ata tgc cgc ttt 513
Ser Ala Pro Asn Tyr Pro Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe
80 85 90
gga tac cag atg gat gaa agc aac caa tgt gtg gat gtg gac gag tgt 561
Gly Tyr Gln Met Asp Glu Ser Asn Gln Cys Val Asp Val Asp Glu Cys
95 100 105
gca aca gat tcc cac cag tgc aac ccc acc cag atc tgc atc aat act 609
Ala Thr Asp Ser His Gln Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr
110 115 120
gaa ggc ggg tac acc tgc tcc tgc acc gac gga tat tgg ctt ctg gaa 657
Glu Gly Gly Tyr Thr Cys Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu
125 130 135 140
ggc cag tgc tta gac att gat gaa tgt cgc tat ggt tac tgc cag cag 705
Gly Gln Cys Leu Asp Ile Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln
145 150 155
ctc tgt gcg aat gtt cct gga tcc tat tct tgt aca tgc aac cct ggt 753
Leu Cys Ala Asn Val Pro Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly
160 165 170
ttt acc ctc aat gag gat gga agg tct tgc caa gat gtg aac gag tgt 801
Phe Thr Leu Asn Glu Asp Gly Arg Ser Cys Gln Asp Val Asn Glu Cys

175 180 185
gcc acc gag aac ccc tgc gtg caa acc tgc gtc aac acc tac ggc tct 849
Ala Thr Glu Asn Pro Cys Val Gln Thr Cys Val Asn Thr Tyr Gly Ser
190 195 200
ttc atc tgc cgc tgt gac cca gga tat gaa ctt gag gaa gat ggc gtt 897
Phe Ile Cys Arg Cys Asp Pro Gly Tyr Glu Leu Glu Glu Asp Gly Val
205 210 215 220
cat tgc agt gat atg gac gag tgc agc ttc tct gag ttc ctc tgc caa 945
His Cys Ser Asp Met Asp Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln
225 230 235
cat gag tgt gtg aac cag ccc ggc aca tac ttc tgc tcc tgc cct cca 993
His Glu Cys Val Asn Gln Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro
240 245 250
ggc tac atc ctg ctg gat gac aac cga agc tgc caa gac atc aac gaa 1041
Gly Tyr Ile Leu Leu Asp Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu
255 260 265
tgt gag cac agg aac cac acg tgc aac ctg cag cag acg tgc tac aat 1089
Cys Glu His Arg Asn His Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn
270 275 280
tta caa ggg ggc ttc aaa tgc atc gac ccc atc cgc tgt gag gag cct 1137
Leu Gln Gly Gly Phe Lys Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro
285 290 295 300
tat ctg agg atc agt gat aac cgc tgt atg tgt cct gct gag aac cct 1185
Tyr Leu Arg Ile Ser Asp Asn Arg Cys Met Cys Pro Ala Glu Asn Pro
305 310 315
ggc tgc aga gac cag ccc ttt acc atc ttg tac cgg gac atg gac gtg 1233

Gly Cys Arg Asp Gln Pro Phe Thr Ile Leu Tyr Arg Asp Met Asp Val
320 325 330
gtg tca gga cgc tcc gtt ccc gct gac atc ttc caa atg caa gcc acg 1281
Val Ser Gly Arg Ser Val Pro Ala Asp Ile Phe Gln Met Gln Ala Thr
335 340 345
acc cgc tac cct ggg gcc tat tac att ttc cag atc aaa tct ggg aat 1329
Thr Arg Tyr Pro Gly Ala Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn
350 355 360
gag ggc aga gaa ttt tac atg cgg caa acg ggc ccc atc agt gcc acc 1377
Glu Gly Arg Glu Phe Tyr Met Arg Gln Thr Gly Pro Ile Ser Ala Thr
365 370 375 380
ctg gtg atg aca cgc ccc atc aaa ggg ccc cgg gaa atc cag ctg gac 1425
Leu Val Met Thr Arg Pro Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp
385 390 395
ttg gaa atg atc act gtc aac act gtc atc aac ttc aga ggc agc tcc 1473
Leu Glu Met Ile Thr Val Asn Thr Val Ile Asn Phe Arg Gly Ser Ser
400 405 410
gtg atc cga ctg cgg ata tat gtg tcg cag tac cca ttc tgagcctcg 1522
Val Ile Arg Leu Arg Ile Tyr Val Ser Gln Tyr Pro Phe
415 420 425
gctggaggcct ccgacgctgc ctctcattgg caccaaggga caggagaaga gaggaaataa 1582
cagagagaat gagagcgaca cagacgttag gcatttcctg ctgaacgttt ccccgaagag 1642
tcagccccga cttcctgact ctcacctgta ctattgcaga cctgtcaccc tgcaggactt 1702
gccaccccca gttcctatga tacagttatc aaaaagtatt atcattgctc ccctgataga 1762
agattgttgg tgaattttca aggccttcag tttatttcaa ctatttcaa agaaaaataga 1822
ttaggtttgc ggggtctga gtctatgttc aaagactgtg aacagcttgc tgtcacttct 1882

tcacctttc cactccttct ctcactgtgt tactgctttg caaagacccg ggagctggcg 1942
ggaaaccctg ggagtagcta gtttgcttt tgcgtacaca gagaaggcta tgtaaacaaa 2002
ccacagcagg atcgaagggt ttttagagaa tgtgtttcaa aaccatgcct ggtattttca 2062
accataaaag aagtttcagt tgtccttaaa tttgtataac ggtttaattc tgtcttggtc 2122
atttttagta tttttaaaaa atatgtcgta gaattcccttc gaaaggcctt cagacacatg 2182
ctatgttctg tcttcccaa cccagtcctcc tctccattt agcccaagtgt tttcttgag 2242
gacccttaa tcttgctttc tttagaattt ttacccaattt ggattggaat gcagaggct 2302
ccaaactgat taaatattt aagaga 2328

<210> 14

<211> 423

<212> PRT

<213> Homo sapiens

<400> 14

Gln Cys Thr Asn Gly Phe Asp Leu Asp Arg Gln Ser Gly Gln Cys Leu

1 5 10 15

Asp Ile Asp Glu Cys Arg Thr Ile Pro Glu Ala Cys Arg Gly Asp Met

20 25 30

Met Cys Val Asn Gln Asn Gly Gly Tyr Leu Cys Ile Pro Arg Thr Asn

35 40 45

Pro Val Tyr Arg Gly Pro Tyr Ser Asn Pro Tyr Ser Thr Pro Tyr Ser

50 55 60

Gly Pro Tyr Pro Ala Ala Ala Pro Pro Leu Ser Ala Pro Asn Tyr Pro

65 70 75 80

Thr Ile Ser Arg Pro Leu Ile Cys Arg Phe Gly Tyr Gln Met Asp Glu
85 90 95
Ser Asn Gln Cys Val Asp Val Asp Glu Cys Ala Thr Asp Ser His Gln
100 105 110
Cys Asn Pro Thr Gln Ile Cys Ile Asn Thr Glu Gly Gly Tyr Thr Cys
115 120 125
Ser Cys Thr Asp Gly Tyr Trp Leu Leu Glu Gly Gln Cys Leu Asp Ile
130 135 140
Asp Glu Cys Arg Tyr Gly Tyr Cys Gln Gln Leu Cys Ala Asn Val Pro
145 150 155 160
Gly Ser Tyr Ser Cys Thr Cys Asn Pro Gly Phe Thr Leu Asn Glu Asp
165 170 175
Gly Arg Ser Cys Gln Asp Val Asn Glu Cys Ala Thr Glu Asn Pro Cys
180 185 190
Val Gln Thr Cys Val Asn Thr Tyr Gly Ser Phe Ile Cys Arg Cys Asp
195 200 205
Pro Gly Tyr Glu Leu Glu Asp Gly Val His Cys Ser Asp Met Asp
210 215 220
Glu Cys Ser Phe Ser Glu Phe Leu Cys Gln His Glu Cys Val Asn Gln
225 230 235 240
Pro Gly Thr Tyr Phe Cys Ser Cys Pro Pro Gly Tyr Ile Leu Leu Asp
245 250 255
Asp Asn Arg Ser Cys Gln Asp Ile Asn Glu Cys Glu His Arg Asn His
260 265 270
Thr Cys Asn Leu Gln Gln Thr Cys Tyr Asn Leu Gln Gly Gly Phe Lys
275 280 285

Cys Ile Asp Pro Ile Arg Cys Glu Glu Pro Tyr Leu Arg Ile Ser Asp
290 295 300
Asn Arg Cys Met Cys Pro Ala Glu Asn Pro Gly Cys Arg Asp Gln Pro
305 310 315 320
Phe Thr Ile Leu Tyr Arg Asp Met Asp Val Val Ser Gly Arg Ser Val
325 330 335
Pro Ala Asp Ile Phe Gln Met Gln Ala Thr Thr Arg Tyr Pro Gly Ala
340 345 350
Tyr Tyr Ile Phe Gln Ile Lys Ser Gly Asn Glu Gly Arg Glu Phe Tyr
355 360 365
Met Arg Gln Thr Gly Pro Ile Ser Ala Thr Leu Val Met Thr Arg Pro
370 375 380
Ile Lys Gly Pro Arg Glu Ile Gln Leu Asp Leu Glu Met Ile Thr Val
385 390 395 400
Asn Thr Val Ile Asn Phe Arg Gly Ser Ser Val Ile Arg Leu Arg Ile
405 410 415
Tyr Val Ser Gln Tyr Pro Phe
420

<210> 15

<211> 1269

<212> DNA

<213> Homo sapiens

<400> 15

cagtgcacga atggcttga cctggatcgc cagtcaggac agtgttaga tattgatgaa 60
tgccgaacca tccccgaggc ctgccgagga gacatgatgt gtgttaacca aatggcggg 120
tatttatgca ttccccggac aaaccctgtg tatcgagggc cctactcgaa cccctactcg 180
acccctact caggtccgta cccagcagct gccccaccac tctcagctcc aaactatccc 240
acgatctcca ggcctttat atgcccgtt ggataccaga tggatgaaag caaccaatgt 300
gtggatgtgg acgagtgtgc aacagattcc caccagtgc acccccacca gatctgcac 360
aatactgaag gcgggtacac ctgctcctgc accgacggat attggcttct ggaaggccag 420
tgcttagaca ttgatgaatg tcgctatggt tactgccagc agctctgtgc gaatgttcct 480
ggatcctatt ctgtacatg caaccctggc tttaccctca atgaggatgg aaggtcttgc 540
caagatgtga acgagtgtgc caccgagaac ccctgcgtgc aaacctgcgt caacacctac 600
ggctcttca tctggcgctg tgacccagga tatgaacttg aggaagatgg cgttcattgc 660
agtgatatgg acgagtgcag cttctctgag ttcctctgcc aacatgagtg tgtgaaccag 720
cccgacat acttctgctc ctgccttca ggctacatcc tgctggatga caaccgaagc 780
tgccaagaca tcaacgaatg tgagcacagg aaccacacgt gcaacctgca gcagacgtgc 840
tacaatttac aagggggctt caaatgcac gacccatcc gctgtgagga gccttatctg 900
aggatcagtg ataaccgctg tatgtgtcct gctgagaacc ctggctgcag agaccagccc 960
tttaccatct tgtaccggga catggacgtg gtgtcaggac gctccgttcc cgctgacatc 1020
ttccaaatgc aagccacgac ccgctaccct ggggcctatt acatttcca gatcaaatct 1080
ggaaatgagg gcagagaatt ttacatgcgg caaacgggcc ccatcagtgc caccctggc 1140
atgacacgcc ccatcaaagg gccccggaa atccagctgg acttggaaat gatcaactgtc 1200
aacactgtca tcaacttcag aggcaagctcc gtgatccgac tgccgatata tgtgtcgcag 1260
tacccattc 1269

<210> 16

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 16

cgattgaatt ctagacctgc ctcgagnnnn nnnnn

35

<210> 17

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:mA55-R1 Primer

<400> 17

cgttgtgca ctgctgctgt gcattcc

27